

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____

Source: _____

Date Processed by STIC: _____

10/577,775

IF400

05/11/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/efb/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/577, 775

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules~~

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,775

TIME: 11:21:12

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577775.raw

3 <110> APPLICANT: KIM, TAE-YOON
 4 BIO CLUE & SOLUTION CO., LT
 6 <120> TITLE OF INVENTION: EC SOD and Cell transducing EC SOD and use thereof
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/577,775
 C--> 8 <141> CURRENT FILING DATE: 2006-04-28
 W--> 0 <130> FILE REFERENCE:
 8 <150> PRIOR APPLICATION NUMBER: KR10-2003-0076629
 9 <151> PRIOR FILING DATE: 2003-10-31
 11 <160> NUMBER OF SEQ ID NOS: 33
 13 <170> SOFTWARE: KopatentIn 1.71

Does Not Comply
 Corrected Diskette Needed
 (pg-1, 2, 3)

ERRORED SEQUENCES

479 <210> SEQ ID NO: 22
 480 <211> LENGTH: 243
 481 <212> TYPE: PRT
 482 <213> ORGANISM: Artificial Sequence
 484 <220> FEATURE:
 485 <223> OTHER INFORMATION: PEP1-EC SOD
 488 <400> SEQUENCE: 22

E--> 490 Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
 491 Lys Lys Arg Lys Val Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser
 E--> 492 Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile
 E--> 494 Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly Thr Leu His Ala
 E--> 496 Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg
 E--> 498 Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu
 E--> 500 Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser
 E--> 502 Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys
 E--> 504 Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln
 E--> 506 His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp
 E--> 508 Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile
 E--> 510

Handwritten notes and corrections:

- 243 OK (with arrow pointing to length 243)
- Invalid Response. What is the source of genetic material. Pls see item # 11 on Error Summary Sheet. (with arrow pointing to PEP1-EC SOD)
- Sequence corrections with handwritten numbers: 1265, 13110, 13615, 14120, 14625, 15130, 1565, 16140, 16645, 17150, 17655, 18160, 18665, 19170, 19675, 20180, 20685, 21190, 21695, 221100, 226101, 231105, 236110, 241115, 246120, 251125, 256130, 261135, 266140, 271145, 276150, 281155, 286160, 291165, 296170

RAW SEQUENCE LISTING

DATE: 05/11/2006

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577775.raw

```

511 Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp Asp Leu Gly Arg
E--> 512 301 175 306 180 311 185
513 Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu
E--> 514 316 190 321 200 326 205
515 Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln
E--> 516 331 210 336 215 341 220
517 Ala Arg Glu His Ser Glu Arg Lys Lys Arg Arg Arg Glu Ser Glu Cys
E--> 518 346 225 351 230 356 235 361 240
519 Lys Ala Ala
523 <210> SEQ ID NO: 23
524 <211> LENGTH: 230
525 <212> TYPE: PRT
526 <213> ORGANISM: Artificial Sequence
528 <220> FEATURE:
529 <223> OTHER INFORMATION: PEP1-deltaHD/EC SOD
532 <400> SEQUENCE: 23
533 Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
E--> 534 123 1 127 5 132 10 137 15
535 Lys Lys Arg Lys Val Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser
E--> 536 142 147 152
537 Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile
E--> 538 157 162 167
539 Trp Gln Glu Val Met Gln Arg Asp Asp Asp Gly Thr Leu His Ala
E--> 540 172 177 182
541 Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg
E--> 542 187 192 197 202
543 Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu
E--> 544 207 212 217
545 Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser
E--> 546 222 227 232
547 Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys
E--> 548 237 242 247
550 Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln
E--> 551 252 257 262
552 His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp
E--> 553 267 272 277 282
554 Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile
E--> 555 287 292 297
556 Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp Asp Leu Gly Arg
E--> 557 302 307 312
558 Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu
E--> 559 317 322 327
560 Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln
E--> 561 332 337 342
562 Ala Arg Glu His Ser Glu
E--> 563 347 352
706 <210> SEQ ID NO: 33
707 <211> LENGTH: 20
708 <212> TYPE: DNA

```

Invalid
Amino Acid
numbering

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,775

TIME: 11:21:12

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577775.raw

709 <213> ORGANISM: Artificial Sequence

711 <220> FEATURE:

712 <223> OTHER INFORMATION: primer

715 <400> SEQUENCE: 33

716 tccaccaccc tggtgctgta

20

E--> 722 2² → delete

VERIFICATION SUMMARY

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,775

TIME: 11:21:13

Input Set : A:\Sequence Listing.txt

Output Set : N:\CRF4\05112006\J577775.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:490 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:492 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:494 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:496 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:498 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:502 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:504 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:506 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:508 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:510 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:512 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:514 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:516 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:518 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:534 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:536 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:538 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:540 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:546 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:548 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:551 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:555 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:557 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:559 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:561 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:563 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:722 M:254 E: No. of Bases conflict, this line has no nucleotides.